RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/889,379_
Source: _Pu/09_
Date Processed by STIC: _1/24/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002
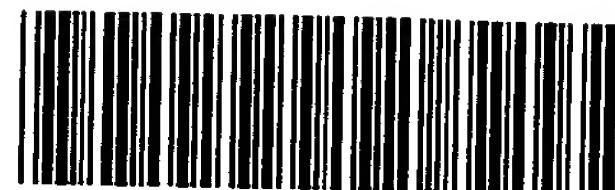
Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: _09/889 399_ |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____ Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____ Use of <220>

Sequence(s) _1-4_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT09

RAW SEQUENCE LISTING   DATE: 01/24/2002
PATENT APPLICATION: US/09/889,379   TIME: 12:26:55

Input Set : A:\56212 sequence listing.txt
Output Set: N:\CRF3\01242002\I889379.raw

```
       3 <110> APPLICANT: Japan Science And Technology Corporation
W-->   4 <120> TITLE OF INVENTION: Method for screening biologically active pyrrole-imidazole
derivatives.
W-->   5 <130> FILE REFERENCE: PA902087
       7 <140> CURRENT APPLICATION NUMBER: US/09/889,379
       7 <141> CURRENT FILING DATE: 2001-12-10
       7 <160> NUMBER OF SEQ ID NOS: 4
      10 <210> SEQ ID NO: 1
      11 <211> LENGTH: 27
      12 <212> TYPE: DNA
      13 <213> ORGANISM: Artificial Sequence
W-->  15 <220> FEATURE:
W-->  15 <223> OTHER INFORMATION:
      15 <400> SEQUENCE: 1
      16 ctgacgagca tcacaaaaat cgacgct                                      27
      19 <210> SEQ ID NO: 2
      20 <211> LENGTH: 27
      21 <212> TYPE: DNA
      22 <213> ORGANISM: Artificial Sequence
W-->  24 <220> FEATURE:
W-->  24 <223> OTHER INFORMATION:
      24 <400> SEQUENCE: 2
      25 agcgtcgatt tttgtgatgc tcgtcag                                      27
      28 <210> SEQ ID NO: 3
      29 <211> LENGTH: 450
      30 <212> TYPE: DNA
      31 <213> ORGANISM: Unknown
W-->  33 <220> FEATURE:
W-->  33 <223> OTHER INFORMATION:
      33 <400> SEQUENCE: 3
      34 agaatcaggg gataacgcag gaaagaacat gtgagcaaaa ggccagcaaa aggccaggaa    60
      35 ccgtaaaaag gccgcgttgc tggcgttttt ccataggctc cgcccccctg acgagcatca   120
      36 caaaaatcga cgctcaagtc agaggtggcg aaacccgaca ggactataaa gataccaggc   180
      37 gtttccccct ggaagctccc tcgtgcgctc tcctgttccg accctgccgc ttaccggata   240
      38 cctgtccgcc tttctccctt cgggaagcgt ggcgctttct caatgctcac gctgtaggta   300
      39 tctcagttcg gtgtaggtcg ttcgctccaa gctgggctgt gtgcacgaac ccccgttca   360
      40 gcccgaccgc tgcgccttat ccggtaacta tcgtcttgag tccaacccgg taagacacga   420
      41 cttatcgcca ctggcagcag ccactggtaa                                    450
      44 <210> SEQ ID NO: 4
      45 <211> LENGTH: 450
      46 <212> TYPE: DNA
      47 <213> ORGANISM: Unknown
W-->  49 <220> FEATURE:
W-->  49 <223> OTHER INFORMATION:
```

RAW SEQUENCE LISTING   DATE: 01/24/2002
PATENT APPLICATION: **US/09/889,379**   TIME: 12:26:55

Input Set : **A:\56212 sequence listing.txt**
Output Set: **N:\CRF3\01242002\I889379.raw**

```
49 <400> SEQUENCE: 4
50 ttaccagtgg ctgctgccag tggcgataag tcgtgtctta ccgggttgga ctcaagacga      60
51 tagttaccgg ataaggcgca gcggtcgggc tgaacggggg gttcgtgcac acagcccagc     120
52 ttggagcgaa cgacctacac cgaactcaga tacctacagc gtgagcattg agaaagcgcc     180
53 acgattcccg aagggagaaa ggcggacagg tatccggtaa gcggcagggt cggaacagga     240
54 gagcgcacga gggagcttcc aggggggaaac gcctggtatc tttatagtcc tgtcgggttt     300
55 cgccacctct gacttgagcg tcgatttttg tgatgctcgt caggggggcg gagcctatgg     360
56 aaaaacgcca gcaacgcggc ctttttacgg ttcctggcct tttgctggcc ttttgctcac     420
57 atgttctttc ctgcgttatc ccctgattct                                      450
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/889,379

DATE: 01/24/2002
TIME: 12:26:56

Input Set : **A:\56212 sequence listing.txt**
Output Set: **N:\CRF3\01242002\I889379.raw**

```
L:4  M:283 W: Missing Blank Line separator, <120> field identifier
L:5  M:283 W: Missing Blank Line separator, <130> field identifier
L:7  M:270 C: Current Application Number differs, Replaced Current Application No
L:7  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:15 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:24 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:24 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:33 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:33 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:49 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:49 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
```